



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/502,510
Source: RET
Date Processed by STIC: 8-2-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/502,510

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 X Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 08/02/2004

PATENT APPLICATION: US/10/502,510

TIME: 09:29:16

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08022004\J502510.raw

3 <110> APPLICANT: El-Gewely, Mohamed Raafat
 4 Gardner, Rebecca
 6 <120> TITLE OF INVENTION: Methods of screening molecular libraries and active
 molecules identified
 7 thereby

W--> 8 <130> FILE REFERENCE: 59.68.75763/001
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/502,510
 C--> 10 <141> CURRENT FILING DATE: 2004-07-23

**Does Not Comply
 Corrected Diskette Needed**

10 <150> PRIOR APPLICATION NUMBER: PCT/GB03/00291
 11 <151> PRIOR FILING DATE: 2003-01-03
 13 <160> NUMBER OF SEQ ID NOS: 51
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 21
 19 <212> TYPE: PRT

C--> 20 <213> ORGANISM: artificial/unknown

*see item 10 on error
 summary sheet.*

22 <220> FEATURE:
 23 <221> NAME/KEY: UNSURE
 24 <222> LOCATION: (1)..(21)
 25 <223> OTHER INFORMATION: secretion signal peptide
 28 <400> SEQUENCE: 1
 30 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 31 1 5 10 15
 33 Gly Ser Thr Gly Asp
 34 20

36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 49
 38 <212> TYPE: PRT
 C--> 39 <213> ORGANISM: artificial/unknown

41 <220> FEATURE:
 42 <221> NAME/KEY: UNSURE
 43 <222> LOCATION: (1)..(49)
 44 <223> OTHER INFORMATION: transmembrane domain
 47 <400> SEQUENCE: 2
 49 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
 50 1 5 10 15
 52 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
 53 20 25 30
 55 Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
 56 35 40 45
 58 Arg

61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 5
 63 <212> TYPE: PRT

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```

C--> 64 <213> ORGANISM: artificial/unknown
66 <220> FEATURE:
67 <221> NAME/KEY: VARIANT
68 <222> LOCATION: (1)..(5)
69 <223> OTHER INFORMATION: peptide derivative
72 <400> SEQUENCE: 3
74 Met Gly Trp Cys Thr
75 1 5
77 <210> SEQ ID NO: 4
78 <211> LENGTH: 190
79 <212> TYPE: DNA
C--> 80 <213> ORGANISM: artificial/unknown
82 <220> FEATURE:
83 <221> NAME/KEY: misc_feature
84 <222> LOCATION: (1)..(190)
85 <223> OTHER INFORMATION: vector
88 <220> FEATURE:
89 <221> NAME/KEY: variation
90 <222> LOCATION: (1)..(190)
91 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
94 <220> FEATURE:
95 <221> NAME/KEY: variation
96 <222> LOCATION: (1)..(190)
97 <223> OTHER INFORMATION: k= G or T in equal molar ratio
100 <400> SEQUENCE: 4
101 ttgacgcaaa tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctcggtta 60
103 gtgaaccgtc agatctctag aagctgggta ccagctgcta gcaagcttgc tagcggccgc 120
105 tgcaggccgg caaggccgga tccagacatg ataagataca ttgatgagtt tggacaaacc 180
107 acaactagaa 190
110 <210> SEQ ID NO: 5
111 <211> LENGTH: 70
112 <212> TYPE: DNA
C--> 113 <213> ORGANISM: artificial/unknown
115 <220> FEATURE:
116 <221> NAME/KEY: misc_feature
117 <222> LOCATION: (1)..(70)
118 <223> OTHER INFORMATION: vector
121 <220> FEATURE:
122 <221> NAME/KEY: variation
123 <222> LOCATION: (1)..(70)
124 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
127 <220> FEATURE:
128 <221> NAME/KEY: variation
129 <222> LOCATION: (1)..(70)
130 <223> OTHER INFORMATION: k= G or T in equal molar ratio
133 <400> SEQUENCE: 5
W--> 134 aagagctcgg taccaagaag gagtttacat atgggannkn nknkgtgata aggatccaag 60
136 cttgaattca 70
139 <210> SEQ ID NO: 6

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RAW SEQUENCE LISTING

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08022004\J502510.raw

```

140 <211> LENGTH: 23
141 <212> TYPE: DNA
C--> 142 <213> ORGANISM: artificial/unknown
144 <220> FEATURE:
145 <221> NAME/KEY: misc_feature
146 <222> LOCATION: (1)..(23)
147 <223> OTHER INFORMATION: synthetic sequence
150 <400> SEQUENCE: 6
151 aagagctcgg taccaagaag gag 23
154 <210> SEQ ID NO: 7
155 <211> LENGTH: 25
156 <212> TYPE: DNA
C--> 157 <213> ORGANISM: artificial/unknown
159 <220> FEATURE:
160 <221> NAME/KEY: misc_feature
161 <222> LOCATION: (1)..(25)
162 <223> OTHER INFORMATION: synthetic sequence
165 <400> SEQUENCE: 7
166 ctgaattcaa gcttggatcc ttatc 25
169 <210> SEQ ID NO: 8
170 <211> LENGTH: 20
171 <212> TYPE: DNA
C--> 172 <213> ORGANISM: artificial/unknown same error
174 <220> FEATURE:
175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (1)..(20)
177 <223> OTHER INFORMATION: primer
180 <400> SEQUENCE: 8
181 agagctcggt tagtgaaccg 20
184 <210> SEQ ID NO: 9
185 <211> LENGTH: 20
186 <212> TYPE: DNA
C--> 187 <213> ORGANISM: artificial/unknown
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (1)..(20)
192 <223> OTHER INFORMATION: primer
195 <400> SEQUENCE: 9
196 gtggtttgtc caaactcatc 20
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 55
201 <212> TYPE: DNA
C--> 202 <213> ORGANISM: artificial/unknown
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (1)..(55)
207 <223> OTHER INFORMATION: library sequence
210 <400> SEQUENCE: 10
211 ggtaccaaga aggagtttac atatgggatg gtgtacttga taaggatcca agctt 55

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RAW SEQUENCE LISTING

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08022004\J502510.raw

214 <210> SEQ ID NO: 11
215 <211> LENGTH: 20
216 <212> TYPE: DNA
C--> 217 <213> ORGANISM: artificial/unknown
219 <220> FEATURE:
220 <221> NAME/KEY: misc_feature
221 <222> LOCATION: (1)..(20)
222 <223> OTHER INFORMATION: primer
225 <400> SEQUENCE: 11
226 ctacctcagg cagctcaagc 20
229 <210> SEQ ID NO: 12
230 <211> LENGTH: 20
231 <212> TYPE: DNA
C--> 232 <213> ORGANISM: artificial/unknown
234 <220> FEATURE:
235 <221> NAME/KEY: misc_feature
236 <222> LOCATION: (1)..(20)
237 <223> OTHER INFORMATION: primer
240 <400> SEQUENCE: 12
241 agacagcacc ctcacatgc 20
244 <210> SEQ ID NO: 13
245 <211> LENGTH: 20
246 <212> TYPE: DNA
C--> 247 <213> ORGANISM: artificial/unknown same error
249 <220> FEATURE:
250 <221> NAME/KEY: misc_feature
251 <222> LOCATION: (1)..(20)
252 <223> OTHER INFORMATION: primer
255 <400> SEQUENCE: 13
256 tgggtgctcat cttaatggcc 20
259 <210> SEQ ID NO: 14
260 <211> LENGTH: 20
261 <212> TYPE: DNA
C--> 262 <213> ORGANISM: artificial/unknown
264 <220> FEATURE:
265 <221> NAME/KEY: misc_feature
266 <222> LOCATION: (1)..(20)
267 <223> OTHER INFORMATION: primer
270 <400> SEQUENCE: 14
271 tgacaaaacc taacttgccg 20
274 <210> SEQ ID NO: 15
275 <211> LENGTH: 26
276 <212> TYPE: DNA
C--> 277 <213> ORGANISM: artificial/unknown
279 <220> FEATURE:
280 <221> NAME/KEY: misc_feature
281 <222> LOCATION: (1)..(26)
282 <223> OTHER INFORMATION: primer
285 <400> SEQUENCE: 15

RAW SEQUENCE LISTING

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08022004\J502510.raw

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286 aagcagtggg aacaacgcag agtact
289 <210> SEQ ID NO: 16
290 <211> LENGTH: 23
291 <212> TYPE: DNA
C--> 292 <213> ORGANISM: artificial/unknown
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (1)..(23)
297 <223> OTHER INFORMATION: primer
300 <400> SEQUENCE: 16
301 aagcagtggg aacaacgcag agt
304 <210> SEQ ID NO: 17
305 <211> LENGTH: 34
306 <212> TYPE: DNA
C--> 307 <213> ORGANISM: artificial/unknown
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <222> LOCATION: (1)..(34)
312 <223> OTHER INFORMATION: primer
315 <400> SEQUENCE: 17
316 atctaagctt gaggttcag cccgggaatt ccag
319 <210> SEQ ID NO: 18
320 <211> LENGTH: 34
321 <212> TYPE: DNA
C--> 322 <213> ORGANISM: artificial/unknown Same error
324 <220> FEATURE:
325 <221> NAME/KEY: misc_feature
326 <222> LOCATION: (1)..(34)
327 <223> OTHER INFORMATION: primer
330 <400> SEQUENCE: 18
331 atctaccggg gccagcagtg ggcgcgtcca acag
334 <210> SEQ ID NO: 19
335 <211> LENGTH: 31
336 <212> TYPE: DNA
C--> 337 <213> ORGANISM: artificial/unknown
339 <220> FEATURE:
340 <221> NAME/KEY: misc_feature
341 <222> LOCATION: (1)..(31)
342 <223> OTHER INFORMATION: primer
345 <400> SEQUENCE: 19
346 aataaccggg gtcgccacca tggtagcaa g
349 <210> SEQ ID NO: 20
350 <211> LENGTH: 34
351 <212> TYPE: DNA
C--> 352 <213> ORGANISM: artificial/unknown
354 <220> FEATURE:
355 <221> NAME/KEY: misc_feature
356 <222> LOCATION: (1)..(34)
357 <223> OTHER INFORMATION: primer

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\08022004\J502510.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 37,38,40,41,43,44
Seq#:42; N Pos. 37,38,40,41,43,44
Seq#:51; Xaa Pos. 2

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

Output Set : N:\CRF4\08022004\J502510.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:39 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:64 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:80 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:113 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:142 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:157 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:172 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:202 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:217 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:232 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:247 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:262 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:277 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:292 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:307 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:322 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:337 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:352 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:367 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:382 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:397 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:412 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:427 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:442 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:457 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:472 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:487 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:502 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:517 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:532 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:547 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:562 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:577 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:592 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:607 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:622 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:637 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:652 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:668 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:684 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:713 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43

VERIFICATION SUMMARY

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Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\08022004\J502510.raw

L:728 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:743 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:758 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:773 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:788 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
L:803 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49
L:818 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0